

# SEQUENCE LISTING

<110> Svendsen, Allan  
Minning, Stefan

<120> Protease Variants

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<170> PatentIn version 3.3

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Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr	
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Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr	
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Ser Lys Ala Phe Thr Gly Thr Gly Lys Val Asn Glu Thr Lys Glu Lys	
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tac	aga	gcg	atc	gtt	cat	att	tca	agc	agc	atc	ggt	tca	tgc	acc	gga	384
Tyr	Arg	Ala	Ile	Val	His	Ile	Ser	Ser	Ser	Ile	Gly	Ser	Cys	Thr	Gly	
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tgg	atg	atc	ggt	cgg	aaa	acc	gtc	gca	aca	gcc	gga	cac	tgc	atc	tat	432
Trp	Met	Ile	Gly	Pro	Lys	Thr	Val	Ala	Thr	Ala	Gly	His	Cys	Ile	Tyr	
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Asp	Thr	Ser	Ser	Gly	Ser	Phe	Ala	Gly	Thr	Ala	Thr	Val	Ser	Pro	Gly	
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cgg	aac	ggg	aca	agc	tat	cct	tac	ggc	tca	gtt	aaa	tgc	acg	cgc	tac	528
Arg	Asn	Gly	Thr	Ser	Tyr	Pro	Tyr	Gly	Ser	Val	Lys	Ser	Thr	Arg	Tyr	
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Ala	Ile	Glu	Leu	Ser	Glu	Pro	Ile	Gly	Asn	Thr	Val	Gly	Tyr	Phe	Gly	
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Tyr	Ser	Tyr	Thr	Thr	Ser	Ser	Leu	Val	Gly	Thr	Thr	Val	Thr	Ile	Ser	
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ggc	tac	cca	ggc	gat	aaa	aca	gca	ggc	aca	caa	tgg	cag	cat	tca	gga	720
Gly	Tyr	Pro	Gly	Asp	Lys	Thr	Ala	Gly	Thr	Gln	Trp	Gln	His	Ser	Gly	
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Pro	Ile	Ala	Ile	Ser	Glu	Thr	Tyr	Lys	Leu	Gln	Tyr	Ala	Met	Asp	Thr	
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Tyr	Gly	Gly	Gln	Ser	Gly	Ser	Pro	Val	Phe	Glu	Gln	Ser	Ser	Ser	Arg	
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Thr	Asn	Cys	Ser	Gly	Pro	Cys	Ser	Leu	Ala	Val	His	Thr	Asn	Gly	Val	
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Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro  
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Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly  
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Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr  
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Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly  
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Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr  
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Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly  
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Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly  
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Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly  
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Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr  
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Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg  
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Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val  
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Ser	Gly	Ile	Leu	Ser	Pro	Val	Asn	Ala	Thr	Gln	Ala	Glu	Thr	Leu	Thr	
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aaa	tta	aat	aaa	ata	agt	cag	aag	cag	gaa	cca	tca	tat	aaa	cta	gat	141
Lys	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp	
				-85					-80					-75		
gaa	gaa	atg	gat	tat	gtt	cta	att	gat	ttg	gaa	aca	caa	tct	gaa	tcg	189
Glu	Glu	Met	Asp	Tyr	Val	Leu	Ile	Asp	Leu	Glu	Thr	Gln	Ser	Glu	Ser	
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Ile	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr	
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Ser	Leu	Gly	Lys	Val	Gly	His	Gly	Glu	Leu	Glu	Lys	Ile	Asn	Leu	Glu	
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gaa	ttt	cgt	aat	cct	aat	tta	aca	gta	gta	gac	cgg	tta	aca	cgt	aag	333
Glu	Phe	Arg	Asn	Pro	Asn	Leu	Thr	Val	Val	Asp	Pro	Leu	Thr	Arg	Lys	
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cct	att	gaa	caa	aaa	atc	agc	cct	ttt	gtt	gtt	ata	ggc	gat	gat	ggg	381
Pro	Ile	Glu	Gln	Lys	Ile	Ser	Pro	Phe	Val	Val	Ile	Gly	Asp	Asp	Gly	
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Arg	Arg	Gln	Val	Gln	Asn	Thr	Ser	Phe	Met	Pro	Phe	Arg	Ala	Leu	Thr	
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Tyr	Ile	Glu	Phe	Gly	Asn	Leu	Thr	Ser	Thr	Trp	Ser	Cys	Ser	Gly	Gly	
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Val	Ile	Gly	Thr	Asp	Leu	Val	Val	Thr	Asn	Ala	His	Cys	Val	Glu	Gly	
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Ser	Val	Leu	Ala	Gly	Thr	Val	Val	Pro	Gly	Met	Asn	Asn	Ser	Gln	Trp	
			60					65					70			
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Ala	Tyr	Gly	His	Tyr	Arg	Val	Thr	Gln	Ile	Ile	Tyr	Pro	Asp	Gln	Tyr	
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aga	aat	aac	ggt	gct	tca	gag	ttt	gat	tat	gct	ata	ctt	aga	gta	gca	669
Arg	Asn	Asn	Gly	Ala	Ser	Glu	Phe	Asp								

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Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr			
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gga tac ccc ggt gat aaa ata tca gag aca aaa tta att tct ttg tgg			813
Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp			
	140	145	150
gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc			861
Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe			
	155	160	165
tac aat atg gac acc tat ttt ggt caa tca ggt tct cct gta tta aac			909
Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn			
	170	175	180
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Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly			
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Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr			
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Lys	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp
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Glu	Glu	Met	Asp	Tyr	Val	Leu	Ile	Asp	Leu	Glu	Thr	Gln	Ser	Glu	Ser
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Ile	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr
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Tyr Ile Glu Phe Gly Asn Leu Thr Ser Thr Trp Ser Cys Ser Gly Gly  
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Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly  
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Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp  
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Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr  
75 80 85

Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala  
90 95 100

Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser  
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Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr  
120 125 130 135

Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp  
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Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe  
155 160 165

Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn  
170 175 180

Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly  
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 Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser  
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 ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc gcc tcc acc 144  
 Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr  
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 tat gat ccc aac ata aaa att gac aat aac gcc gca tat tcg aaa gcc 192  
 Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala  
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 ttc gaa gga acc gga aca ccc gcc gcc tcc gtt cag gcc aaa ccg aaa 240  
 Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys  
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 aaa gaa tcg ccc gcc gcc ccg cct tac agc cct aaa tcg gta atc gcc 288  
 Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly

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gca atc gtc cat att tca agc agc atc ggc tca tgc aca ggc tgg ctg							384
Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu							
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atc gga ccg aaa acg gta gca acg gcc ggg cac tgc gtc tat gac acg							432
Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr							
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Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn							
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ggt tca gct tac cct tac gga tct gtt aca tcg acc cgc tat ttc atc							528
Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile							
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Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile							
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gag ctg agc cag ccg atc ggc aat acc gtc gga tat ttc gga tat tca							624
Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser							
		105		110		115	
tac acc gct tca tcg ctt gca gga gca ggc gtg acc atc agc gga tat							672
Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr							
	120		125		130		
cca gga gac aaa aca aca ggc acc cag tgg caa atg tcc gga acg atc							720
Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile							
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Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly							
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Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn							
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tgc agc ggc cca tgc tcg ctg gcc gtt cat acg aac ggc gtg tac gga							864
Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly							
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gga tcc tct tac aac aga ggc acc cgc att acg aaa gaa gta ttt gat							912
Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val Phe Asp							
	200		205		210		
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Lys Glu Ser Pro Ala Gly Pro Pro Tyr Ser Pro Lys Ser Val Ile Gly  
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Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Thr Ala Phe Pro Tyr Arg  
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Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr  
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Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn  
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Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile  
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Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile  
 85 90 95 100

Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser  
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 Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile  
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 Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val Tyr Gly  
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Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu						
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acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca						144
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser						
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Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val						
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gat gat cta tct tca act gtt ggt gaa aaa gta aaa cca cta tca aaa						240
Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys						
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tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat ggt aga						288
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg						
	-5		-1 1		5	
aca aaa gta gca aat aca aga gtg gca cca tat aat tca att gct tat						336
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr						
	10		15		20	
act acg ttt ggc ggc tcc agc tgc acg ggg acc ctg att gcc cct aac						384
Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn						
	25		30		35	40
aaa att ttg aca aac gga cac tgc gtg tac aat aca gca tcc aga agt						432
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser						
		45		50		55
tat agt gca aaa gga tgc gtg tat cca ggc atg aat gat agt act gcg						480
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala						
	60		65		70	
gtg aat ggc tca gca aat atg aca gag ttc tat gta cca agc ggg tat						528
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr						
	75		80		85	
atc aat aca ggt gcg agc caa tat gat ttt gcc gtg atc aaa aca gat						576
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp						
	90		95		100	
acg aac att ggc aat aca gtt ggt tac cgt tcc atc cgt cag gtg aca						624
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr						
	105		110		115	120
aac tta act ggc aca acg att aaa att tct gga tat cca ggt gat aaa						672
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys						
		125		130		135
atg aga tca act ggc aag atc tgc cag tgg gag atg tca ggt cct gtg						720
Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val						
	140		145		150	

aca aga gaa gat acg aat ctg gca tac tat atg att gat aca ttt agt 768  
 Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser  
 155 160 165

gga aat tca ggc tca gcg atg cta gat caa aat cag caa att gtt ggg 816  
 Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly  
 170 175 180

gtt cat aac gca ggg tat tca aac ggt acg att aat ggc ggt cca aaa 864  
 Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys  
 185 190 195 200

gcg aca gct gcc ttt gtt gaa ttt atc aac tat gca aaa gcg caa 909  
 Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln  
 205 210 215

<210> 8  
 <211> 303  
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 <213> Bacillus pumilus BO32

<400> 8

Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly  
 -85 -80 -75

Ala Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu  
 -70 -65 -60

Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser  
 -55 -50 -45

Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val  
 -40 -35 -30 -25

Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys  
 -20 -15 -10

Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg  
 -5 -1 1 5

Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr  
 10 15 20

Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn  
 25 30 35 40

Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser  
45 50 55

Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala  
60 65 70

Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr  
75 80 85

Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp  
90 95 100

Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr  
105 110 115 120

Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys  
125 130 135

Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val  
140 145 150

Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser  
155 160 165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly  
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys  
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln  
205 210 215

<210> 9  
<211> 954  
<212> DNA  
<213> Bacillus licheniformis CDJ31

<220>  
<221> CDS  
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<220>  
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<222> (1)..(84)

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<222> (85)..(288)

<220>
<221> mat_peptide
<222> (289)..(954)

<400> 9
atg aaa aaa agt gtg aca cgc gta tta atg gcc ggt ctt att gga ata      48
Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
-95 -90 -85

tct att tat tct atg ggc atc gac tcc gct caa gct gca tca tcg ccg      96
Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
-80 -75 -70 -65

cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca     144
His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
-60 -55 -50

agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa     192
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
-45 -40 -35

gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa     240
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys
-30 -25 -20

agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa     288
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys
-15 -10 -5 -1

tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca     336
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala
1 5 10 15

tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc     384
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys
20 25 30

acc ggc tcc ctg atc ggt ccg aaa acg gtg gca acg gcc gga cac tgc     432
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys
35 40 45

att tat gac aca gcg agc ggg tca ttc gcc gga acc gct acc gtt tct     480
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser
50 55 60

ccg gga cgg aac ggt tca aca tat ccg tac gga tca gtt aca tca acc     528
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr
65 70 75 80

cgc tat ttc atc ccg tca ggc tat cga agc gga aat tcg aat tac gac     576
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
85 90 95

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tac gga gcc ata gag ctc agc cag ccg atc ggc aac acc gtc ggg tat	624
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr	
100 105 110	

ttc gga tat tcc tac acc acc tcg tot ctc gtt ggg tca agc gtt acc	672
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr	
115 120 125	

atc atc gga tat cca ggc gac aaa aca tcg ggc acc caa tgg cag atg	720
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met	
130 135 140	

tcc gga aat atc gcc gtc tca gaa aca tat aaa ctg caa tat gcg atc	768
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile	
145 150 155 160	

gac aca tac gga ggg cag agc ggc tct ccc gta tat gag gcg agc agc	816
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser	
165 170 175	

tcc aga acg aat tgc agc ggc cca tgt tcg ctg gcc gtt cat acg aat	864
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn	
180 185 190	

ggg gtg tac gga gga tct tca tac aac aga ggc acc cgg att aca aaa	912
Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys	
195 200 205	

gaa gta ttc gat aat ttg aca aac tgg aaa aac agc gcc caa	954
Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln	
210 215 220	

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 <212> PRT  
 <213> Bacillus licheniformis CDJ31

<400> 10

Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
-95 -90 -85

Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
-80 -75 -70 -65

His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala
-60 -55 -50

Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys
-45 -40 -35

Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys  
           -30                              -25                              -20

Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys  
      -15                              -10                              -5                              -1

Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala  
 1                              5                              10                              15

Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys  
                               20                              25                              30

Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys  
                               35                              40                              45

Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser  
      50                              55                              60

Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr  
 65                              70                              75                              80

Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp  
                               85                              90                              95

Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr  
                               100                              105                              110

Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr  
                               115                              120                              125

Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met  
      130                              135                              140

Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile  
 145                              150                              155                              160

Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser  
                               165                              170                              175

Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn  
                               180                              185                              190

Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys

195

200

205

Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln  
 210 215 220

<210> 11  
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 <212> DNA  
 <213> *Bacillus pumilus* JA96

<220>  
 <221> CDS  
 <222> (1)..(906)

<220>  
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<220>  
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 <222> (76)..(261)

<220>  
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 atg aaa aag gtg aaa aaa tta atc cct tct cta ctc gtt ttt ggt gct 48  
 Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala  
 -85 -80 -75

tta agt gtg cct agt ttt gcc cat gca gca tct gat tca gta ctt acg 96  
 Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr  
 -70 -65 -60

tct gat tat gac atg gtg act tct gac gga aag gtg att tct tca gct 144  
 Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala  
 -55 -50 -45 -40

gac ttc cac aac gat atg aaa acc ccc tca tcc ttt gac aaa gtg gat 192  
 Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp  
 -35 -30 -25

gat ctc tct tct act att ggc gaa aaa gta aaa cca ctc aca aca tat 240  
 Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr  
 -20 -15 -10

tta aaa gac ttt caa aca aaa gta gtc att gga gac gat ggt aga aca 288  
 Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr  
 -5 -1 1 5

aaa gtg acg aat aca aga gta gca ccc tat aat tct att gct tat att 336  
 Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile  
 10 15 20 25

aca ttt ggt gga tct agc tgc act gga aca ctc att gct cca aac aaa	384
Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys	
30 35 40	
ata ttg aca aac gga cac tgc gtc tac aat aca gcc aca aga agt tat	432
Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr	
45 50 55	
agt gca aaa ggg tct gtc tac cca ggc atg aat gac agc acg gct gtg	480
Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val	
60 65 70	
aac ggc tca gca aac atg acc gaa ttc tat gta cca agc gga tat atc	528
Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile	
75 80 85	
aac acg ggg gcg agt caa tat gat ttt gcc gtc att aaa aca gat acg	576
Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr	
90 95 100 105	
aac att gga aat acg gtc ggc tat cgc tct att cgt caa gtg aca aat	624
Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn	
110 115 120	
cta aca ggt aca acg att aaa att tct gga tat cca ggt gat aaa atg	672
Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met	
125 130 135	
aga tcg act ggc aaa gtg tca caa tgg gaa atg tca ggt cca gtc acg	720
Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr	
140 145 150	
aga gaa gat acg aat ctc gca tac tat acg atc gat aca ttt agc gga	768
Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly	
155 160 165	
aac tct ggc tct gcg atg cta gat cag aac caa caa atc gtc ggg gtc	816
Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val	
170 175 180 185	
cat aat gcg ggt tat tca aat gga acg atc aac ggt gga cca aaa gcg	864
His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala	
190 195 200	
act gct gcc ttt gtt gaa ttt atc aac tat gcg aag gcg caa	906
Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln	
205 210 215	

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 <212> PRT  
 <213> Bacillus pumilus JA96

<400> 12

Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala  
-85 -80 -75

Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr  
-70 -65 -60

Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala  
-55 -50 -45 -40

Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp  
-35 -30 -25

Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr  
-20 -15 -10

Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr  
-5 -1 1 5

Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile  
10 15 20 25

Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys  
30 35 40

Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr  
45 50 55

Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val  
60 65 70

Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile  
75 80 85

Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr  
90 95 100 105

Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn  
110 115 120

Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met  
125 130 135

Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr

140                      145                      150  
 Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly  
     155                      160                      165  
 Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val  
     170                      175                      180                      185  
 His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala  
                     190                      195                      200  
 Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln  
                     205                      210                      215

<210> 13  
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 <212> DNA  
 <213> Bacillus subtilis IS75

<220>  
 <221> CDS  
 <222> (1)..(939)

<220>  
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<220>  
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<220>  
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 atg aaa tta gtt cca aga ttc aga aaa caa tgg ttc gct tac tta acg 48  
 Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr  
                     -90                      -85                      -80  
 gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca 96  
 Val Leu Cys Leu Ala Leu Ala Ala Val Ser Phe Gly Val Pro Ala  
                     -75                      -70                      -65  
 aaa gcg gca gag aac ccg caa act tct gta tcg aat acc ggt aaa gaa 144  
 Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu  
                     -60                      -55                      -50  
 gct gat gct acg aaa aac caa acg tca aaa gca gat cag gtt tcc gcc 192  
 Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala  
                     -45                      -40                      -35                      -30

cct tat gag gga acc gga aaa aca agt aaa tcg tta tac ggc ggc caa Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln -25 -20 -15	240
acg gaa ctg gaa aaa aac att caa acc tta cag cct tcg agc att atc Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile -10 -5 -1 1	288
gga act gat gaa cgc acc aga atc tcc agc acg aca tct ttt cca tat Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr 5 10 15	336
aga gca acc gtt caa ctg tca atc aag tat ccc aac act tca agc act Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr 20 25 30 35	384
tat gga tgt acc gga ttt tta gtc aat cca aat aca gtc gtc acg gct Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala 40 45 50	432
gga cat tgt gtg tac agc cag gat cat gga tgg gct tcg acg ata acc Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr 55 60 65	480
gcc gcg ccg ggc cgc aat ggt tcg tca tat ccg tac ggt act tat tca Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser 70 75 80	528
ggc acg atg ttt tac tcc gtc aaa gga tgg acg gaa agc aaa gac acc Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr 85 90 95	576
aac tat gat tac gga gct att aaa tta aac ggt tct cct gga aac acg Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr 100 105 110 115	624
gtt ggc tgg tac ggc tac cgg act aca aac agc agc agt ccc gtg ggc Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly 120 125 130	672
ctt tcc tcg tca gtg aca gga ttc cca tgt gac aaa acc ttt ggc acg Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr 135 140 145	720
atg tgg tct gat aca aag ccg att cgc tcc gct gaa acg tat aag ctg Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu 150 155 160	768
acc tat aca acc gat acg tac ggc tgc caa agc ggc tcg cct gtt tat Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr 165 170 175	816
cga aac tac agt gat aca ggg cag aca gct att gcc att cac acg aac Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn 180 185 190 195	864

gga gga tgg tca tat aac ttg gga aca agg gtg acg aac gat gta ttc 912  
 Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe  
                   200                  205                  210

aac aat att caa tat tgg gca aat caa 939  
 Asn Asn Ile Gln Tyr Trp Ala Asn Gln  
                   215                  220

<210> 14  
 <211> 313  
 <212> PRT  
 <213> Bacillus subtilis IS75

<400> 14

Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr  
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Val Leu Cys Leu Ala Leu Ala Ala Ala Val Ser Phe Gly Val Pro Ala  
                   -75                  -70                  -65

Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu  
                   -60                  -55                  -50

Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala  
                   -45                  -40                  -35                  -30

Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln  
                   -25                  -20                  -15

Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile  
                   -10                  -5                  -1 1

Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr  
                   5                  10                  15

Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr  
                   20                  25                  30                  35

Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala  
                   40                  45                  50

Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr  
                   55                  60                  65

Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser

70	75	80
Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr		
85	90	95
Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr		
100	105	110
Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly		
	120	125
		130
Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr		
	135	140
		145
Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu		
	150	155
		160
Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr		
	165	170
		175
Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn		
180	185	190
		195
Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe		
	200	205
		210
Asn Asn Ile Gln Tyr Trp Ala Asn Gln		
	215	220

<210> 15  
 <211> 909  
 <212> DNA  
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<220>  
 <221> CDS  
 <222> (1)..(909)

<220>  
 <221> sig\_peptide  
 <222> (1)..(78)

<220>  
 <221> pro\_peptide  
 <222> (79)..(264)

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<220>
<221> mat_peptide
<222> (265)..(909)

<400> 15
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Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
          -85                      -80                      -75

gct tta agt gtg cct agt ttt gcc cat gcc aca tcg gat tca gta cta      96
Ala Leu Ser Val Pro Ser Phe Ala His Ala Thr Ser Asp Ser Val Leu
          -70                      -65                      -60

acg tct gat tat gac atg gtg act tct gat gga aag gtg atc tct tca     144
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
          -55                      -50                      -45

agt gat ttc cac aat gat acg aaa tcc ccc tca tcc ttt gac aaa gtg     192
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
          -40                      -35                      -30                      -25

gat gat ctt tot tct act tct ggc gaa aaa gta aaa cca ctc tca aaa     240
Asp Asp Leu Ser Ser Thr Ser Gly Glu Lys Val Lys Pro Leu Ser Lys
          -20                      -15                      -10

tat tta aaa gac ttt caa aca aaa gtc gtc att gga gac gat gga ada     288
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Xaa
          -5                      -1 1                      5

aca aaa gta gca aac aca aga gtg gca cca tat aat tca att gct tat     336
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
          10                      15                      20

att aca ttt ggc ggc tca agc tgc acg ggg aca ctc att gcc cct aac     384
Ile Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
          25                      30                      35                      40

aaa att ttg aca aac ggg cac tgc gtg tac aat aca gca tcg aga agt     432
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
          45                      50                      55

tat agt gca aaa gga tcg gtg tat cca ggc atg aac gat agt aca gcg     480
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
          60                      65                      70

gtg aat ggc tca gca aac atg acg gag ttc tat gta cca agc gga tat     528
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
          75                      80                      85

atc aat aca ggc gcg agc caa tat gat ttt gcc gtg atc aaa aca gat     576
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
          90                      95                      100

acg aac att ggc aat acg gtc ggt tac cgc tot atc cgt cag gtg aca     624
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
          105                      110                      115                      120

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aac tta act ggg aca acg att aaa att tct gga tat cca ggt gat aaa	672
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys	
125 130 135	
atg ada tcg act ggc aag gtg tcg cad tgg gag atg tca ggt tct gtg	720
Met Xaa Ser Thr Gly Lys Val Ser Xaa Trp Glu Met Ser Gly Ser Val	
140 145 150	
aca aga gaa gat aca aat ctc gca tac tat acg att gat aca ttt agc	768
Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser	
155 160 165	
gga aat tca ggc tca gcg atg cta gat caa aat cad caa atc gtt ggg	816
Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Xaa Gln Ile Val Gly	
170 175 180	
gtt cat aac gca ggg tat tca aac gga acg att aat ggc ggt cca aaa	864
Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys	
185 190 195 200	
gcg aca gct gcc ttt gtt gaa ttt atc aac tat gca aaa gcg caa	909
Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln	
205 210 215	

<210> 16  
 <211> 303  
 <212> PRT  
 <213> Bacillus intermedius

<220>  
 <221> misc\_feature  
 <222> (8)..(8)  
 <223> The 'Xaa' at location 8 stands for Lys, Arg, or Ile.

<220>  
 <221> misc\_feature  
 <222> (138)..(138)  
 <223> The 'Xaa' at location 138 stands for Lys, Arg, or Ile.

<220>  
 <221> misc\_feature  
 <222> (145)..(145)  
 <223> The 'Xaa' at location 145 stands for Gln, or His.

<220>  
 <221> misc\_feature  
 <222> (180)..(180)  
 <223> The 'Xaa' at location 180 stands for Gln, or His.

<400> 16

Met Met Lys Lys Val Lys Met Leu Leu Pro Ser Leu Leu Val Phe Gly
-85 -80 -75

Ala Leu Ser Val Pro Ser Phe Ala His Ala Thr Ser Asp Ser Val Leu

-70		-65		-60
Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser				
-55		-50		-45
Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val				
-40		-35		-30
Asp Asp Leu Ser Ser Thr Ser Gly Glu Lys Val Lys Pro Leu Ser Lys				
	-20		-15	-10
Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Xaa				
-5		-1 1		5
Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr				
10		15		20
Ile Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn				
25		30		35
Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser				
	45		50	55
Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala				
	60		65	70
Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr				
	75		80	85
Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp				
90		95		100
Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr				
105		110		115
Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys				
	125		130	135
Met Xaa Ser Thr Gly Lys Val Ser Xaa Trp Glu Met Ser Gly Ser Val				
	140		145	150
Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser				
155		160		165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Xaa Gln Ile Val Gly  
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys  
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln  
205 210 215

<210> 17  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Primer

<400> 17  
ctgtgccctt taaccgcaca gc 22

<210> 18  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Primer

<400> 18  
gcataagctt ttacaggtac cggc 24